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NURBS CURVE FITTING USING ARTIFICIAL IMMUNE SYSTEM

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Abstract. *Non-Uniform Rational B-spline (NURBS) is an industrial standard for Computer Aided Design (CAD) model data representation. For constructing an CAD model from a physical part by curve modeling and dimensional measure, the NURBS design often results in a multi-objective optimization (MOO) problem which cannot be handled as such by traditional single objective optimization algorithms. For large data, this problem needs to be dealt with non-deterministic optimization algorithms achieving global optimum and at the same time getting to the desired solution in an iterative fashion. In order to find a good NURBS model from large number of data, generally the knots, control points and weights are respected as variables. In this paper, the minimization of the fitting error is aimed in order to find a smooth curve and the optimization of the NURBS weights and the knot vector for curve fitting is worked. The heuristic of Artificial Immune System (AIS) was used as a new methodology. The best model was searched among the candidate models by using the Akaike's Information Criteria (AIC). Numerical examples were given in order to show the efficiency of our method.*
Keywords: Curve approximation, Artificial immune system, NURBS, Control points, Knots

1. **Introduction.** Curve fitting is widely used in applications of many fields such as image processing, computer graphics, industrial and computer-aided design (CAD) and computer-aided manufacturing (CAM) for vector-based drawing, font design, data reduction, approximating noisy data, curve and surface fairing, visualization and approximation. Recently, researchers have spent considerable time figuring out how best to fit curves to a set of data points. Although researchers used analytical function for curve fitting the input data, since the shape of the underlying function of data is frequently complicated, it is difficult to approximate it by a single polynomial. In this case, an appropriate spline model and its variants are the most appropriate approximating functions [1]. Non-uniform rational B-splines (NURBSs) have various useful properties such as smoothness and the possibility of local modifications, which facilitate the representation of general freeform surfaces. These properties of NURBS are ideal for the design of complicated geometry, making them a standard tool in computer-aided design and manufacturing (CAD/CAM). A kth degree B-spline curve is uniquely defined by its control points and knot values, but for NURBS curves, the weight vector has to be specified [2].

Since the NURBSs consist of multi-parameters, control points, knots and weights, the rational format of the objective function makes the fitting task a multi-variable nonlinear optimization problem. Although various algorithms exist for nonlinear optimization problems, they are usually computationally expensive and time consuming. A good non-deterministic optimization strategy may be a candidate to be applied to gain optimal approximation results.

The current paper concentrates only on weight parameters and knots vector to be optimized so that optimal NURBS curve model can be achieved efficiently for 2D data. This paper presents the application with two phases of one of the computational intelligence techniques called "Artificial Immune System (AIS)" to the curve fitting problem by using NURBS. Individuals are formed by treating knot placement candidates in first phase and weights of the NURBS in second phase as antibody and the continuous problem is solved as a discrete problem as in [3]. By using Akaike Information Criteria (AIC), affinity criterion is described and the search is implemented from the good candidate models towards the best model in each generation. The result of the optimization process is set of NURBS curves of arbitrary degree.

2. Literature Survey.

As NURBSs have several control handlers (control points, knot vectors and weights), designers have to decide among themselves to select the parameters to vary and get the desired shapes. This is one of the most important issues in Computer Graphics [5], Computer Aided Geometric Design (CAGD) [6], and CAD/CAM. In [7], the weights or control points were recomputing. Various interpolation schemes for NURBS curves have been developed by Farin [8] for conics that a special case of NURBS curves. In [9], approximate estimation of the knot values and optimization of values of points has been made. In [10], simulation of various facial expressions in animation is performed by fixing the control points and changing weights, while in [11], optimization of the knot vector for multi-curve B-spline approximation is performed. Some other researchers investigated nonlinear approaches for NURBS curve and surface approximation. A typical approaoch can be found in [12]. It identifies both the control points and the weights of a NURBS curve/surface simultaneously by minimizing the sum of the squares of the distances between the measured points and fitted curve/surface points. A similar approach is also reported in [13]. In addition to the weights and the control points, the knots are also considered as unknowns in [13]. In addition, a two-step linear approach was reported in [14]. During the first step, the weights are identified from a homogeneous system. The control points are further solved.

Direct search methods have also been used for the weights and knot optimization. The search methods have the advantage of rapid convergence, but on the other hand may linger in local minima. In [15], it used binary-coded Genetic Algorithm (GA)'s for control point optimization and then knot values optimization, and the error minimization of parametric surfaces as a global optimization problem is shown. In a similar way using GA, in [1,16], optimization of both the knots and the weights corresponding to the control points for curve and surface fitting is done. Sarfraz [17] is used Simulated Annealing heuristic for the weight optimization of NURBS for visualization of data. The objective of the method is to visualize data by reducing the error and to obtain a smooth curve. Then in [18], in addition to independent studies of the optimization of weight and knot parameters of the NURBS, a separate scheme has also been developed for the optimization of weights and knots simultaneously.

AIS is used for the optimization of the knots of the B-spline surfaces in Ülker's previous work [3]. However, in this paper, for optimizing the NURBS parameters, AIS global optimization heuristic is applied by extended previous work with the optimization of the weights.

3. The Curve Fitting with NURBS.

3.1. NURBS curve. A NURBS curve is the rational combination of a set of piecewise basis functions with n control points p_i and their associated weights w_i:

$$c(u) = \frac{\sum_{i=0}^{n} p_i w_i N_{i,k}(u)}{\sum_{i=0}^{n} w_i N_{i,k}(u)} \tag{1}$$

where u is the parametric variable, $p(u) = [x(u), y(u), z(u)]^T \in R^3$ represents a point on the NURBS curve at parameter u and $N_{i,k}(u)$ are the normalized B-spline basis functions of k degree. The normalized B-splines that can be uniquely defined by an order k, the number of control points n, and a set of $n+k$ knots t_i. The weight w_i determines the influence of the ith control vector P_i on the curve. The ith basis function $N_{i,p}(u)$ defined on a knot vector $U = \{t_0, t_1, \ldots, t_{n+k+1}\}$ is recursively defined by using uniform knots.

$$\begin{aligned} N_{i,1}(u) &= \begin{cases} 1 & \text{for } t_i \le u < t_{i+1} \\ 0 & \text{otherwise} \end{cases} \\ N_{i,k}(u) &= \frac{u - t_i}{t_{i+k-1} - t_i} N_{i,k-1}(u) + \frac{t_{i+k} - u}{t_{i+k} - t_{i+1}} N_{i+1,k-1}(u) \end{aligned} \tag{2}$$

The parametric domain is $t_k \le u \le t_{n+1}$. The non-periodic knot vector customarily has the form $U = \{\alpha, \ldots, \alpha, u_{k+1}, \ldots, u_n, \beta, \ldots, \beta\}$ in which α and β appear $(k+1)$ times at the ends. This special arrangement at the ends guarantees that the initial and final control points, respectively, coincide with the initial and final data points. Throughout in this paper, we assume that the parameter lies in the range $u \in [0, 1]$. Thus, $\alpha = 0$ and $\beta = 1$.

3.2. Invers design. To optimize the NURBS curve for the given digital data, the computation of control points to be used in NURBS, will be computed through non-uniform B-spline (NUBS), which is the non-rational counter part of the NURBS. To determine a NURBS curve interpolating $(n+1)$ data points $\{Q_k\}$ it suffices to have $(n+1)$ independent conditions. If a data point lies on a B-spline curve, then it must satisfy Equation (1). If we assign a parameter value $\overline{u_k}$ to each data point, and select a knot vector U and a weight vector W, we can set up the curve interpolation problem as follows.

$$Q_k = C(\overline{u_k}) = \sum_{i=0}^{n} P_i R_{i,k}(\overline{u_k}) \quad k = 0, \ldots, n \tag{3}$$

or can set up in matrix form as follows.

$$\begin{gathered} \begin{bmatrix} R_{0,p}(\overline{u_0}) & \cdots & R_{m,p}(\overline{u_0}) \\ R_{0,p}(\overline{u_1}) & \cdots & R_{m,p}(\overline{u_1}) \\ \vdots & \ddots & \vdots \\ R_{0,p}(\overline{u_n}) & \cdots & R_{m,p}(\overline{u_n}) \end{bmatrix} \begin{bmatrix} P_0 \\ P_1 \\ \vdots \\ P_n \end{bmatrix} = \begin{bmatrix} Q_0 \\ Q_1 \\ \vdots \\ Q_n \end{bmatrix} \\ \text{or} \\ [C][P] = [Q] \end{gathered} \tag{4}$$

where the rational functions $\{R_{i,k}(u)\}$ are defined by

$$R_{i,k}(u) = \frac{w_i N_{i,k}(u)}{\sum_{i=0}^{m} w_i N_{i,k}(u)} \tag{5}$$

Although there are many ways to determine the parameter value $\overline{u_k}$, the uniform method, chord length method and centripetal method are well preferred. For the chord length and centripetal methods, the knot vector U is defined as follows.

$$\begin{aligned} &U = \{0,\, 0,\, \ldots,\, 0,\, u_{k+1},\, \ldots,\, u_n,\, 1,\, 1,\, \ldots,\, 1\} \\ &u_{j+k} = \frac{1}{k} \sum_{i=j}^{j+k-1} \overline{u_i} \quad \text{for } j = 1, \ldots, n-k \end{aligned} \tag{6}$$

Using the basis polygon matrice that was created Equation (4) the defining polygon vertices of control points for a B-spline curve is calculated from the data points $\{Q_k\}$ as follows:

$$[P] = [C]^T\, [C]^{-1}\, [C]^T\, [Q] \tag{7}$$

3.3. **Curve fitting with NURBS.** Given a set of data points F in the plane, we compute a planar NURBS curve to approximate the points. This curve is called the target curve or the target shape. For generalization, let us assume that is the measurement error between the fitted curve and the target curve. So, we can write [18].

$$F\,(t) = f\,(t) + \varepsilon\,(t) \tag{8}$$

where t represents the parameter. In the above equation, $f(t)$ is the underlying function which is to be approximated using NURBS and $\varepsilon(t)$ represents the measurement error at the particular value of t at that data point.

Let us assume that the number of the control points is n and the degree of the NURBS is k (order $k+1$). For parameter t in data fitting, the knot vector is constructed by using the centripetal method in Equation (6). The control points are calculated by using the obtained knots vector and Equation (7). Later Equation (4) is fitting to data given by Equation (8) for fit the NURBS curve to the set of given data points. Then the sum of squares of residuals by using Equation (9) (in this work, $r = 2$).

The error function (or cost/objective function) between the measured points and the fitted curve is generally given by the following equation [18]:

$$E = \left(\sum_{i=0}^{s} \left| Q_i - S\,(\alpha_1, \ldots, \alpha_n) \right|^r / s \right)^{1/r} \tag{9}$$

where Q represents the set of measured points; $S\,(\alpha_1, \ldots, \alpha_n)$ is the geometric model of the fitted curve, where $(\alpha_1, \ldots, \alpha_n)$ are the parameters of the fitted curve; s is the number of measured points and r is an exponent, ranging from 1 to infinity. The fitting task can then be viewed as the optimization of the curve parameters to minimize the error (or cost) E. If exponent r is equal to 2, the above equation reduces to the least squares function.

4. **The Proposed Artificial Immune System Approach.** De Castro et al. [19] propounded Clonal Selection Algorithm as taking the operations in maturation of affinity as base and they analyzed the performance of their algorithm by applying it to the problems like character recognition and optimization. For the NURBS curve fitting, the original problem converted into a discrete combinatorial optimization problem like in [1,3]. Then, the converted problem was solved by the Clonal Selection Algorithm of AIS.

The system is formed by units called as Antigen (Ag) and Antibody (Ab) in immune system. The interactions between Antigen and Antibody are modeled by an affinity scale. A distance scale is used as a criterion or measurement scale. The distances between Antigens and Antibodies can be calculated with varieties of methods. If antibody and antigen are represented as $Ab = \langle Ab_1, Ab_2, \ldots, Ab_L \rangle$ and $Ag = \langle Ag_1, Ag_2, \ldots, Ag_L \rangle$, respectively, Euclid distance between Ab and Ag is calculated by Equation (10).

$$D = \sqrt{\sum_{i=1}^{L} (Ab_i - Ag_i)^2} \tag{10}$$

NURBS fitting problem is to approximate the NURBS curve that approximate a target (object) curve in a certain tolerance interval. Assume that object curve is defined as N grid type with ordered and dense points in 2D space and the knots of the NURBS curve that will be fitted are n grid that is subset of N grid. Degrees of curves, k, will be entered from the user. Given number of points N is assigned to L that is dimensions of the Antigen and Antibody that are using for the representation the both the knots and the NURBS weights and creating by a bit string. Each bit of Antibody and Antigen is also called their molecule and is equivalent to a data point. If the value of a molecule is 1 in this formulation then a knot is placed to a suitable data point otherwise no knot is placed (Figure 1). Initially, the weight vector created by 1's (or 100's). If the given points are lied down between $[a, b]$ intervals, n items of knots are defined in this interval and called as *interior knots*. Initial population includes K Antibody with L numbers of molecules. Molecules are set as 0 and 1, randomly. The molecule set that includes the numbers and places of the interior knots that define NURBS/B-spline with maximum fitting to data points with minimum error is Antigen that must be defined. These knots determine the control points needed to approximate the underlying curve outline. Since we are applying NURBS, the weights associated with these control points are also to be optimized. The number of elements in the weights vector correspond to the number of the control points. Therefore the problem is consist of two search spaces at the same time. One search space is related to the optimization of the interior knots, while the other one to the positive weights associated with the calculated control points. The weights consist of antibodies consisting of numbers and without 1's and 0's, which can be positive real or integers, e.g.,

10 45 67 98 34 99

represents a valid antibody in this study. This dual space search in makes this algorithm a "*Nested Clonal Selection Algorithm*". The flow-chart based on the Clonal Selection for

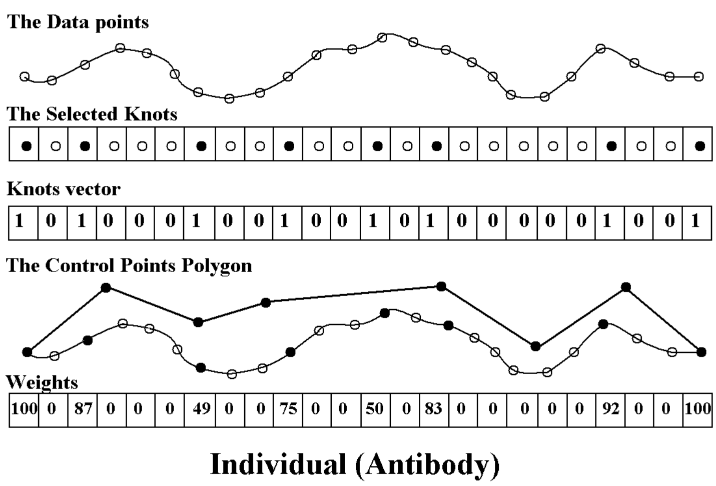


FIGURE 1. The antibody by knots and weights

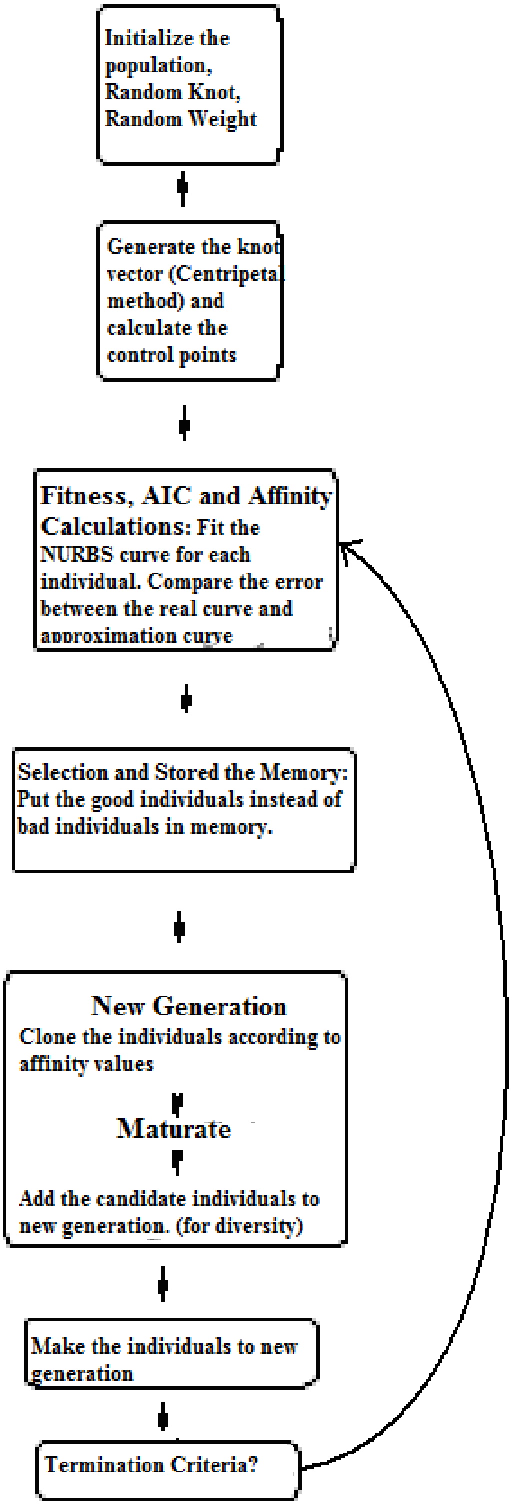


FIGURE 2. The flow-chart of the curve fitting system with NURBS

NURBS curve fitting is shown in Figure 2. For provide the interpolation at two end-points, first and last points are conserved in the initial population and the subsequent ones in order to prevent our AIS algorithm form losing these points during cloning and maturate operations. In the clonal selection algorithm, their conservation is achieved by applying an OR operation of the whole population with the antibody having ones only at the end point locations only. The operation is performed just after a new population is formed after cloning and maturate operations.

In the present study, minimum distance for maximum interaction method was used for interactions between Antigen and Antibody. Euclid distance scale in Equation (10) is used as criterion or measure for determining the degree of the interactions of cells of Antigen-Antibody. In order to response against Antigen, Antibody must recognize them. In our study, the affinity of antibodies to antigens is determined in terms of distance between the antigen and the antibody and also Akaike's Information Criterion (AIC) which is preferred as a fitness measure in references [1,3]. This formula for recognition process is as follows.

$$Affinity = 1 - \left(\frac{AIC}{AIC_{avrg}}\right) \tag{11}$$

where AIC_{avrg} represents the arithmetical average of AIC values of all Antibodies in the population and calculated as follow. If the AIC value of any of the individual is greater than AIC_{avrg} then Affinity is accepted as zero (Affinity = 0) in Equation (12).

$$AIC_{avrg} = \frac{\sum_{i=1}^{K} AIC_i}{K} \tag{12}$$

where K is the size of the population and AIC_i is the fitness measure of the ith antibody in the population. AIC is given as below.

$$AIC = N \log_e E + 2\,(2n + m) \tag{13}$$

where N represents the number of data, n represents number of interior knots, m represents the order of the spline fitted on the data and E is calculated by Equation (10). Equation (13) is used as fitness measure in both the knots optimization and the weight optimization. It should be taken into account that antibody with the highest affinity is the one with lower error. The antibody which is ideal solution and the exact complementary of the Antigen is the one whose affinity value is nearest to 1 among the population (in fact in memory). Euclid distance between ideal Antibody and Antigen is equal to zero. In this case, the problem becomes not curve approximation but curve interpolation.

Before trying to find out a solution to the problem, certain control parameters must be entered into the program. These are order of the curve, population size, memory size, variety ratio and mutation ratio. Memory size is given as the double of the population size as preference. Inside of the memory, the best antibodies of the whole iterations till the current time are kept. The population variety degree is assigned by variety ratio parameter. This value is the ratio of the number of the Antibody whose molecules will be determined randomly to the population size. In the cloning step, cloning is implemented according to the affinity value as suitable to the spirit of AIS. The antibodies with higher affinity are cloned more whereas antibodies with lower affinity are either cloned less or not cloned. Cloned antibodies were applied maturate operation by generally doing double points crossing it with a randomly chosen individual from the memory or changing the molecule order randomly. If the number of clones of an antibody is excessive, both the methods mentioned above lines were applied to clones of it. After a certain number of execution of AIS as iteratively, antibody with the highest affinity against antigen is chosen as solution.

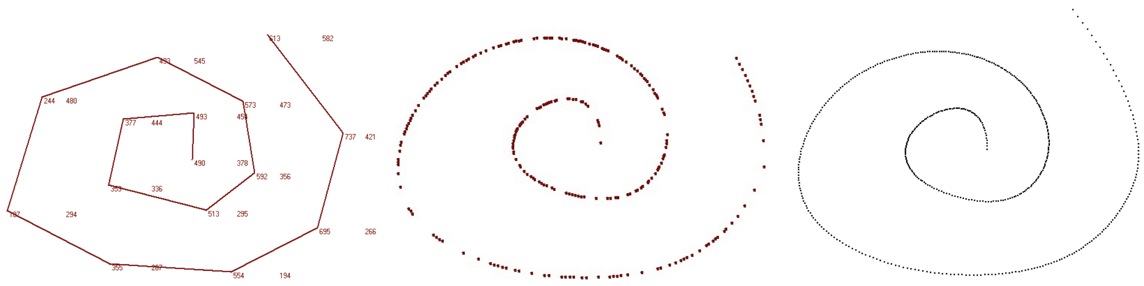
In order to integrate clonal selection algorithm to this problem some modification must be carried out on the original algorithm. The followings are step by step explanation of the modifications made on the algorithm and how these modifications applied to above mentioned algorithm.

1. Enter the data points to be fitted.
2. Enter the control parameters.
3. Build initial Antibody population with random molecules.
4. Implementation the knots optimization by using the algorithm of B-spline curve fitting (as in [3]).
5. Create the antibodies as the NURBS weights and generate initial Antibody population with random molecules.
6. If the population is built as the first time, create memory (the array of Weight_Memory) and save all antibodies in the Weight_Memory.
7. Otherwise, update Weight_Memory cells with the antibody population and develop the Weight_Memory.
8. For each of antibody calculate NURBS by using Equation (3) and fit it to the given curve by using Equation (8). Later on calculate the sum of squares of residuals (E) by using Equation (9).
9. For each of antibody in the population calculate its AIC value (Equation (13)) and calculate the average AIC value of population (Equation (12)).
10. For each of antibody calculate the affinity (Equation (11)).
11. Choose the best antibodies according to the affinity (the euclid distance, Equation (10)) and in request antigen and interactions of every antibody. (in sum, the number of the clones will be K-varieties).
12. Produce matured antibody population by making the molecules change rational with affinity values of clones. (by using Weight_Memory or by change antibody molecules in random).
13. Implement mutation according to the mutation rate.
14. Produce new antibody according to the variety ratio.
15. If iteration limit is not reached or antigen is not recognized fully go to Step (7).
16. Finally, return the best antibody of the Weight_Memory as the best weight.

5. **Experimental Results.** We can make the comparison here by using the results of the earlier GA and AIS knot placement algorithms in which the optimization of the weights is added.

Figure 3 shows an example of B-spline curve parameterization to evaluate proposed AIS-based NURBS curve fitting algorithm. In this work, both the knot optimization and the weight optimization are executed. Sixteen percent noise from uniform distribution was added artificially to a clean data for obtaining the 2D data (200 in number). The intended curve to the modeled is a non uniform B-spline cubic curve with 15 control points and $\{0.0, 0.0, 0.0, 0.0, 0.25, 0.5, 0.75, 1.0, 1.0, 1.0, 1.0\}$ knot vectors. In AIS architecture because of the antibodies which have the most sensitivity are saving in memory content, for every breed the most sensitive antibody of the memory is given in results. The Root Mean Square (RMS) error between the modeled curve and point cloud based on the antibodies in memory population is reported in Table 1. The initial population was bred for 300 generations for Knot Optimization and 55 generations for Knot and Weight Optimization. Figure 3(b) shows the best supplemental antibody in the initial population. Figure 3(c) shows the convergence pattern after 55 (for Knot and Weight Optimization) generations. The curve now conforms better to the data points. The fitness is increases (the error decreases) while the generations are increasing.

To compare performance evaluation and speed of convergence, the compare were done between our algorithm based on AIS and the GA algorithm proposed from Sarfaz et al. [2,16]. In GA algorithm, knot ratio and manual fixing of important points at knot chromosomes are not taken into consideration. Input points are again the data points shown in Figure 3. To evaluate the accuracy, the RMS values obtained from GA method are given at (3th column of) Table 1. Nonetheless, the values of parameters used for both of two algorithms are presented in Table 2. Our AIS based algorithm and GA based algorithm proposed by Safraz et al. are also compared according to speed of convergence. We are getting the program outputs of some generations in training period. According to these outputs, according to population in that generation, average RMS values, maximum RMS values and number of knots of the individuals and antibodies are given in Table 3. According to all generations, the convergence diagrams of our proposed AIS approach and the GA approach are presented in Figure 4 for knot and knot-weight optimization. In this figure, green lines are the maximum fitness values while red lines are the minimum fitness values.



(a) (b) (c)

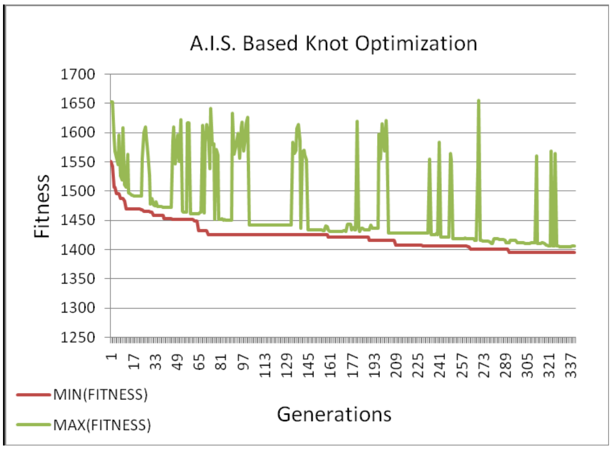
Figure 3. (a) The control polygon of the 2D NURBS data points, (b) the NURBS curve for the best complementary antibody in initial population, (c) the NURBS curve for the convergence antigen after AIS optimization (55 generations)

Table 1. The RMS values of AIS and GA for the example curve shown in Figure 3

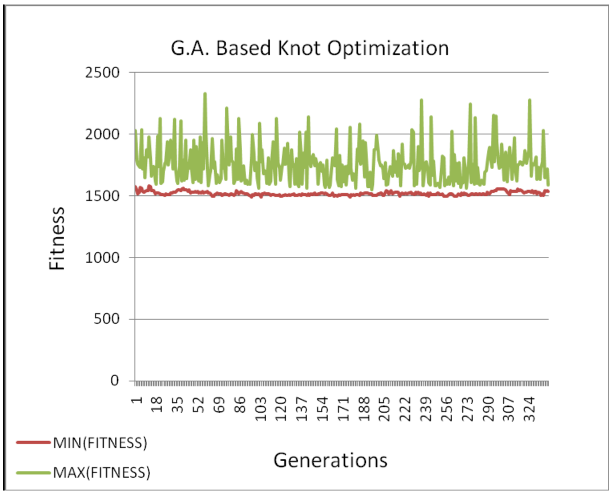
Generation	Knot Opt.				Knot and Weight Opt.	
	AIS		GA		AIS	
	BEST RMS	Knots	BEST RMS	Knots	BEST RMS	Knots
Initial	1.2658	89	2.0300	97	1.3239	105
10	1.2235	88	1.8743	95	1.2123	82
25	1.1335	88	1.7624	102	1.1362	79
50	1.1142	85	1.6299	96	1.0257	82
100	1.1006	84	1.7060	91	none	None
200	1.0884	78	1.8618	93	none	None
300	1.1306	72	1.7212	86	none	None

Table 2. The set of parameters

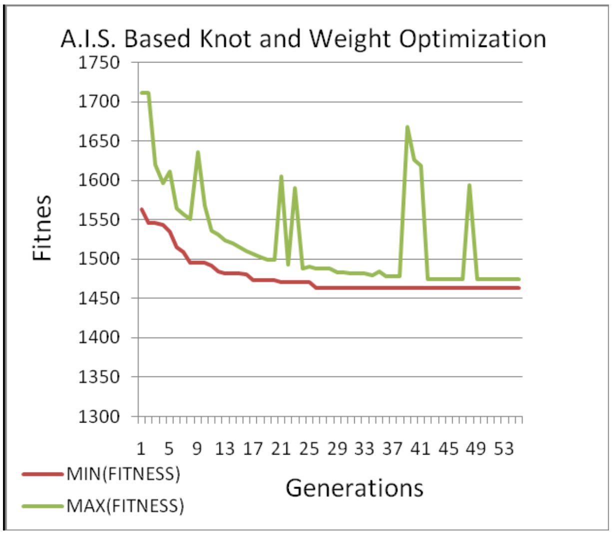
Parametre	AIS	GA
Population size	20	20
String length	200 (Antibody cell length)	200 (chromosome gen-length)
Mutation Rate	None	0.001
Crosover Olasılığı	None	0.7
Cesitlilik Sayisi	6 (30%)	6 (30%)
Memory Size	40	None



(a)



(b)



(c)

FIGURE 4. AIS and GA based parameter optimization according to generations: (a) knot optimization by AIS, (b) knot optimization by GA, (c) knot and weight optimization by AIS

Table 3. RMS statistics of GA knot, AIS knot and AIS knot and weight optimization shown in Figure 4

	G.A. (Knot Opt., 500 generations)			A.I.S. (Knot Opt., 500 generations)			A.I.S. (Knot and Weight Opt., 100 generations)		
	Max RMS	Average RMS	Knots	Max RMS	Average RMS	Knots	Max RMS	Average RMS	Knots
1	4.004	2.598	49	3.936	2.397	56	5.027	3.054	50
10	2.723	2.123	52	2.974	1.802	46	2.348	1.782	56
25	2.951	2.406	58	2.212	1.424	49	2.190	1.590	56
50	3.222	1.935	55	2.203	1.188	47	0.955	0.953	56
100	3.161	2.112	38	2.388	0.972	46	0.911	0.910	56
200	2.890	2.195	54	0.925	0.889	46	none	none	none
300	2.875	2.089	52	0.925	0.889	46	none	none	none
400	2.944	2.070	60	1.005	0.890	46	none	none	none
500	3.105	2.474	44	0.894	0.864	46	none	none	none

As a second case study, data to be fitted are generated by

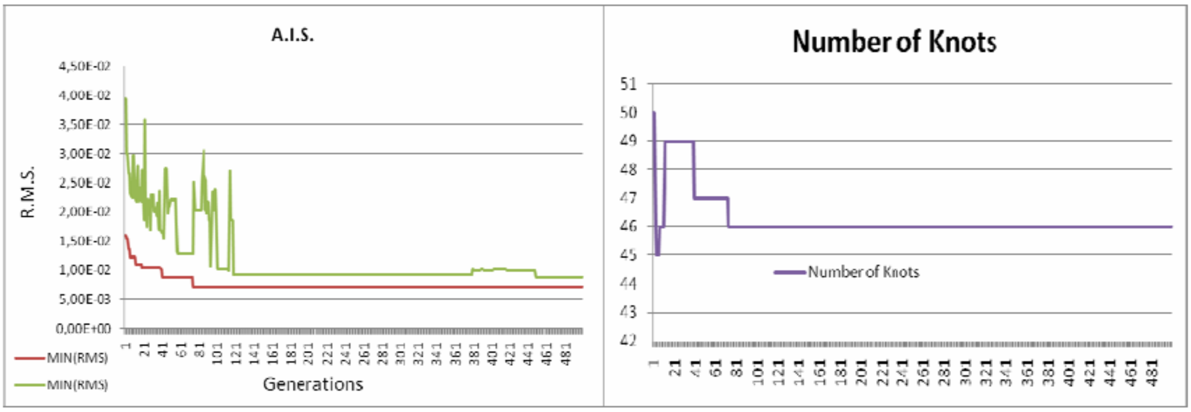
$$F_j = 90/\left(1 + e^{-100(x_j - 0.4)}\right), \quad (j = 1, 2, \cdots, N).$$

where any error value is not used, the values of x_j is $0.0, 0.01, \ldots, 1.0$ and the number of them is 101. The interval of the fitting was set to $[a, b] = [0, 1]$. In GA, the weight optimization does not exist. However, in our method both of them are done. A NURBS (order 4) is used as an approximating function. Our method does not depend on the order of approximating function. Control parameters are the same with the values in Table 2.

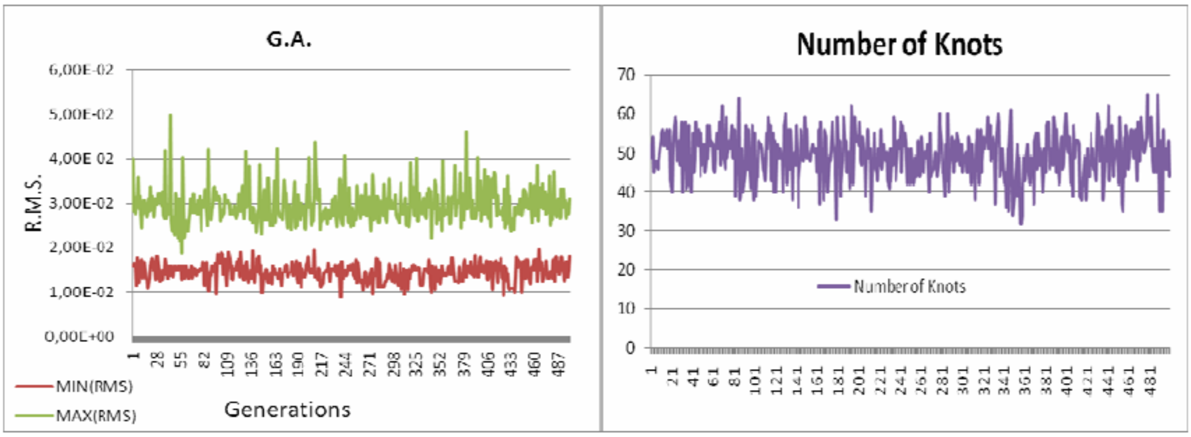
Figure 5 shows the fitness and number of knots against generations. The red line and green line shows the minimum RMS and the maximum RMS, respectively. From the red line, we can see that our computation converged at the 78st generation for knot and weight optimization and it is 0.9087. The blue line is the number of knots for the generations. The number of knots decreases from 56 at the first generation to 47 at the 3th generation for knot and weight optimization. The best RMS value for AIS is 0.8945 obtained at 473th generation and the number of knots is 46 for same generation. The best RMS value for GA is 0.9133 obtained at 426th generation and the number of knots is 47 for same generation.

6. **Conclusions.** In this paper, a multi-objective optimization algorithm was suggested for design by optimization of curves. Optimizing both the knots and the weights of the NURBS model exploits maximal degrees of freedom of the curve and therefore high quality results may be obtained. For least-squares fitting of NURBS curves, a two-step non-deterministic approach is employed. During the first step, the knots vector are defined by selecting the best knots. The control points according to finding knot vector are then established in a similar way to that for a B-spline curve fitting. In second step, the AIS approach is again applied for identifying the weights. Both a general solution and a solution for best-fitting positive weights can be obtained. The performance depends on the parameterization. Since the algorithm can identify the best-fitting or optimal weights, one can therefore use the full power of NURBS.

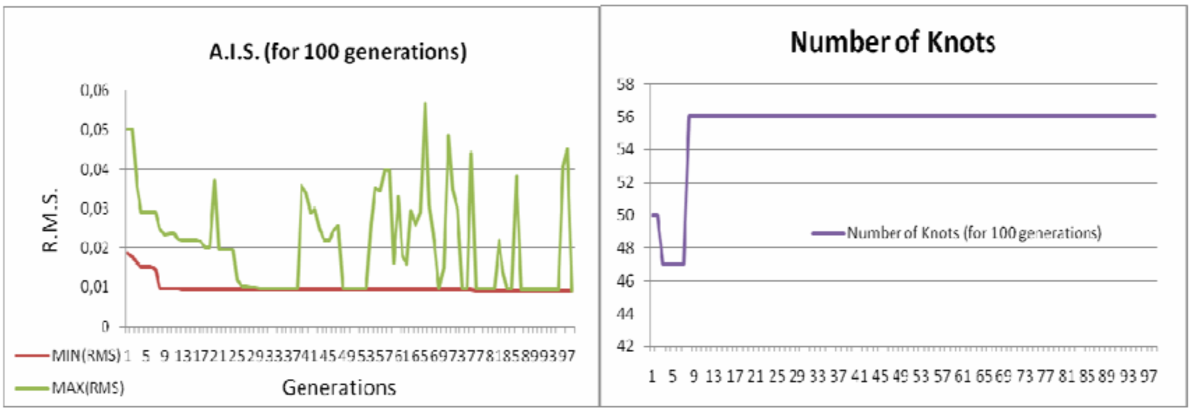
In this paper, it has been clearly shown that proposed AIS algorithm is very useful for determine the best weights of the NURBS and for the recognition of the good knot automatically. Since AIC is used as fitting function in this study, the simplicity of the model can be balanced with adherence of the model to the data and the best model can



(a)



(b)



(c)

FIGURE 5. Graphics of the RMS and number of knots for second case study: (a) AIS (knot optimization, 500 generations), (b) GA (knot optimization, 500 generations), (c) AIS (knot and weight optimization, 100 generations)

be chosen between candidate models as automatically. None of the subjective parameters such as error tolerance or a regularity (order) factor and initial places of the knots that are chosen well are not required.

In future, this work can be extended to optimize other two or more possible NURBS parameters like control point-weight. This study can also be applied to NURBS surfaces instead of NURBS curves. Also, this work can be incorporated in the reverse engineering component of the CAD/CAM modeling software's.

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